

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 09/142,471D  
Source: IFW/b  
Date Processed by STIC: 12/19/05

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IFW16

**RAW SEQUENCE LISTING**

DATE: 12/19/2005

PATENT APPLICATION: US/09/142,471D

TIME: 09:42:46

Input Set : A:\012627-009.txt

Output Set: N:\CRF4\12192005\I142471D.raw

4 <110> APPLICANT: ROSE-JOHN, Stefan  
 5 ANGEWANDTE GENTECHNOLOGIE SYSTEME GMBH  
 7 <120> TITLE OF INVENTION: CONJUGATE FOR MODIFYING INTERACTIONS BETWEEN  
 PROTEINS

9 <130> FILE REFERENCE: 012627-009  
 11 <140> CURRENT APPLICATION NUMBER: 09/142,471D  
 12 <141> CURRENT FILING DATE: 1998-11-04  
 14 <150> PRIOR APPLICATION NUMBER: PCT/DE97/00458  
 15 <151> PRIOR FILING DATE: 1997-03-07  
 17 <150> PRIOR APPLICATION NUMBER: DE 196 08 813.5  
 18 <151> PRIOR FILING DATE: 1996-03-07  
 20 <160> NUMBER OF SEQ ID NOS: 17  
 22 <170> SOFTWARE: PatentIn Ver. 2.0  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 1627  
 26 <212> TYPE: DNA  
 27 <213> ORGANISM: Unknown  
 29 <220> FEATURE:  
 30 <221> NAME/KEY: sig\_peptide  
 31 <222> LOCATION: (34)..(90)  
 33 <220> FEATURE:  
 34 <221> NAME/KEY: mat\_peptide  
 35 <222> LOCATION: (91)..(1608)  
 37 <220> FEATURE:  
 38 <221> NAME/KEY: CDS  
 39 <222> LOCATION: (34)..(1608)  
 41 <220> FEATURE:  
 42 <223> OTHER INFORMATION: Description of Unknown Organism:A conjugate  
 43 comprising two polypeptides with a mutual  
 44 affinity.  
 46 <400> SEQUENCE: 1  
 47 gtcgacgcat ggagtggtag ccgaggagga agc atg ctg gcc gtc ggc tgc gcg 54  
 48 Met Leu Ala Val Gly Cys Ala  
 49 -15  
 51 ctg ctg gct gcc ctg ctg gcc gcg ccg gga gcg gcg ctg gcc cca agg 102  
 52 Leu Leu Ala Ala Leu Leu Ala Ala Pro Gly Ala Ala Leu Ala Pro Arg  
 53 -10 -5 -1 1  
 55 cgc tgc cct gcg cag gag gtg gca aga ggc gtg ctg acc agt ctg cca 150  
 56 Arg Cys Pro Ala Gln Val Ala Arg Gly Val Leu Thr Ser Leu Pro  
 57 5 10 15 20  
 59 gga gac agc gtg act ctg acc tgc ccg ggg gta gag ccg gaa gac aat 198  
 60 Gly Asp Ser Val Thr Leu Thr Cys Pro Gly Val Glu Pro Glu Asp Asn  
 61 25 30 35  
 63 gcc act gtt cac tgg gtg ctc agg aag ccg gct gca ggc tcc cac ccc 246

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64	Ala	Thr	Val	His	Trp	Val	Leu	Arg	Lys	Pro	Ala	Ala	Gly	Ser	His	Pro	
65				40					45					50			
67	agc	aga	tgg	gct	ggc	atg	gga	agg	agg	ctg	ctg	ctg	agg	tcg	gtg	cag	294
68	Ser	Arg	Trp	Ala	Gly	Met	Gly	Arg	Arg	Leu	Leu	Leu	Arg	Ser	Val	Gln	
69			55					60					65				
71	ctc	cac	gac	tct	gga	aac	tat	tca	tgc	tac	cgg	gcc	ggc	cgc	cca	gct	342
72	Leu	His	Asp	Ser	Gly	Asn	Tyr	Ser	Cys	Tyr	Arg	Ala	Gly	Arg	Pro	Ala	
73		70					75					80					
75	ggg	act	gtg	cac	ttg	ctg	gtg	gat	gtt	ccc	ccc	gag	gag	ccc	cag	ctc	390
76	Gly	Thr	Val	His	Leu	Leu	Val	Asp	Val	Pro	Pro	Glu	Glu	Pro	Gln	Leu	
77	85				90				95					100			
79	tcc	tgc	ttc	cgg	aag	agc	ccc	ctc	agc	aat	gtt	gtt	tgt	gag	tgg	ggt	438
80	Ser	Cys	Phe	Arg	Lys	Ser	Pro	Leu	Ser	Asn	Val	Val	Cys	Glu	Trp	Gly	
81				105					110				115				
83	cct	cgg	agc	acc	cca	tcc	ctg	acg	aca	aag	gct	gtg	ctc	ttg	gtg	agg	486
84	Pro	Arg	Ser	Thr	Pro	Ser	Leu	Thr	Thr	Lys	Ala	Val	Leu	Leu	Val	Arg	
85				120					125				130				
87	aag	ttt	cag	aac	agt	ccg	gcc	gaa	gac	ttc	cag	gag	ccg	tgc	cag	tat	534
88	Lys	Phe	Gln	Asn	Ser	Pro	Ala	Glu	Asp	Phe	Gln	Glu	Pro	Cys	Gln	Tyr	
89			135				140				145						
91	tcc	cag	gag	tcc	cag	aag	ttc	tcc	tgc	cag	tta	gca	gtc	ccg	gag	gga	582
92	Ser	Gln	Glu	Ser	Gln	Lys	Phe	Ser	Cys	Gln	Leu	Ala	Val	Pro	Glu	Gly	
93		150				155				160							
95	gac	agc	tct	ttc	tac	ata	gtg	tcc	atg	tgc	gtc	gcc	agt	agt	gtc	ggg	630
96	Asp	Ser	Ser	Phe	Tyr	Ile	Val	Ser	Met	Cys	Val	Ala	Ser	Ser	Val	Gly	
97	165				170				175				180				
99	agc	aag	ttc	agc	aaa	act	caa	acc	ttt	cag	ggt	tgt	gga	atc	ttg	cag	678
100	Ser	Lys	Phe	Ser	Lys	Thr	Gln	Thr	Phe	Gln	Gly	Cys	Gly	Ile	Leu	Gln	
101				185					190				195				
103	cct	gat	ccg	cct	gcc	aac	atc	aca	gtc	act	gcc	gtg	gcc	aga	aac	ccc	726
104	Pro	Asp	Pro	Pro	Ala	Asn	Ile	Thr	Val	Thr	Ala	Val	Ala	Arg	Asn	Pro	
105			200					205					210				
107	cgc	tgg	ctc	agt	gtc	acc	tgg	caa	gac	ccc	cac	tcc	tgg	aac	tca	tct	774
108	Arg	Trp	Leu	Ser	Val	Thr	Trp	Gln	Asp	Pro	His	Ser	Trp	Asn	Ser	Ser	
109			215				220					225					
111	ttc	tac	aga	cta	cgg	ttt	gag	ctc	aga	tat	cgg	gct	gaa	cgg	tca	aag	822
112	Phe	Tyr	Arg	Leu	Arg	Phe	Glu	Leu	Arg	Tyr	Arg	Ala	Glu	Arg	Ser	Lys	
113		230				235					240						
115	aca	ttc	aca	aca	tgg	atg	gtc	aag	gac	ctc	cag	cat	cac	tgt	gtc	atc	870
116	Thr	Phe	Thr	Thr	Trp	Met	Val	Lys	Asp	Leu	Gln	His	His	Cys	Val	Ile	
117	245				250				255				260				
119	cac	gac	gcc	tgg	agc	ggc	ctg	agg	cac	gtg	gtg	cag	ctt	cgt	gcc	cag	918
120	His	Asp	Ala	Trp	Ser	Gly	Leu	Arg	His	Val	Val	Gln	Leu	Arg	Ala	Gln	
121				265					270				275				
123	gag	gag	ttc	ggg	caa	ggc	gag	tgg	agc	gag	tgg	agc	ccg	gag	gcc	atg	966
124	Glu	Glu	Phe	Gly	Gln	Gly	Glu	Trp	Ser	Glu	Trp	Ser	Pro	Glu	Ala	Met	
125			280					285					290				
127	ggc	acg	cct	tgg	aca	gaa	tcc	agg	agt	cct	cca	gct	cga	gga	ggt	gga	1014
128	Gly	Thr	Pro	Trp	Thr	Glu	Ser	Arg	Ser	Pro	Pro	Ala	Arg	Gly	Gly	Gly	

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129          295          300          305
131 ggt tct gga ggt gga ggt tct gga ggt gga ggt tct gtc gag cca gta 1062
132 Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Val Glu Pro Val
133          310          315          320
135 ccc cca gga gaa gat tcc aaa gat gta gcc gcc cca cac aga cag cca 1110
136 Pro Pro Gly Glu Asp Ser Lys Asp Val Ala Ala Pro His Arg Gln Pro
137 325          330          335          340
139 ctc acc tct tca gaa cga att gac aaa caa att cgg tac atc ctc gac 1158
140 Leu Thr Ser Ser Glu Arg Ile Asp Lys Gln Ile Arg Tyr Ile Leu Asp
141          345          350          355
143 ggc atc tca gcc ctg aga aag gag aca tgt aac aag agt aac atg tgt 1206
144 Gly Ile Ser Ala Leu Arg Lys Glu Thr Cys Asn Lys Ser Asn Met Cys
145          360          365          370
147 gaa agc agc aaa gag gca ctg gca gaa aac aac ctg aac ctt cca aag 1254
148 Glu Ser Ser Lys Glu Ala Leu Ala Glu Asn Asn Leu Asn Leu Pro Lys
149          375          380          385
151 atg gct gaa aaa gat gga tgc ttc caa tct gga ttc aat gag gag act 1302
152 Met Ala Glu Lys Asp Gly Cys Phe Gln Ser Gly Phe Asn Glu Glu Thr
153          390          395          400
155 tgc ctg gtg aaa atc atc act ggt ctt ttg gag ttt gag gta tac cta 1350
156 Cys Leu Val Lys Ile Ile Thr Gly Leu Leu Glu Phe Glu Val Tyr Leu
157 405          410          415          420
159 gag tac ctc cag aac aga ttt gag agt agt gag gaa caa gcc aga gct 1398
160 Glu Tyr Leu Gln Asn Arg Phe Glu Ser Ser Glu Glu Gln Ala Arg Ala
161          425          430          435
163 gtg cag atg agt aca aaa gtc ctg atc cag ttc ctg cag aaa aag gca 1446
164 Val Gln Met Ser Thr Lys Val Leu Ile Gln Phe Leu Gln Lys Lys Ala
165          440          445          450
167 aag aat cta gat gca ata acc acc cct gac cca acc aca aat gcc agc 1494
168 Lys Asn Leu Asp Ala Ile Thr Thr Pro Asp Pro Thr Thr Asn Ala Ser
169          455          460          465
171 ctg ctg acg aag ctg cag gca cag aac cag tgg ctg cag gac atg aca 1542
172 Leu Leu Thr Lys Leu Gln Ala Gln Asn Gln Trp Leu Gln Asp Met Thr
173          470          475          480
175 act cat ctc att ctg cgc agc ttt aag gag ttc ctg cag tcc agc ctg 1590
176 Thr His Leu Ile Leu Arg Ser Phe Lys Glu Phe Leu Gln Ser Ser Leu
177 485          490          495          500
179 agg gct ctt cgg caa atg tagcatgggc accgtcgac 1627
180 Arg Ala Leu Arg Gln Met

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181 505

184 &lt;210&gt; SEQ ID NO: 2

185 &lt;211&gt; LENGTH: 525

186 &lt;212&gt; TYPE: PRT

187 &lt;213&gt; ORGANISM: Unknown

189 &lt;220&gt; FEATURE:

190 &lt;223&gt; OTHER INFORMATION: A conjugate comprising two polypeptides with a mutual affinity

192 &lt;400&gt; SEQUENCE: 2

193 Met Leu Ala Val Gly Cys Ala Leu Leu Ala Ala Leu Leu Ala Ala Pro

194 -15

-10

-5

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196 Gly Ala Ala Leu Ala Pro Arg Arg Cys Pro Ala Gln Glu Val Ala Arg
197      -1  1      5      10
199 Gly Val Leu Thr Ser Leu Pro Gly Asp Ser Val Thr Leu Thr Cys Pro
200      15      20      25
202 Gly Val Glu Pro Glu Asp Asn Ala Thr Val His Trp Val Leu Arg Lys
203  30      35      40      45
205 Pro Ala Ala Gly Ser His Pro Ser Arg Trp Ala Gly Met Gly Arg Arg
206      50      55      60
208 Leu Leu Leu Arg Ser Val Gln Leu His Asp Ser Gly Asn Tyr Ser Cys
209      65      70      75
211 Tyr Arg Ala Gly Arg Pro Ala Gly Thr Val His Leu Leu Val Asp Val
212      80      85      90
214 Pro Pro Glu Glu Pro Gln Leu Ser Cys Phe Arg Lys Ser Pro Leu Ser
215      95      100      105
217 Asn Val Val Cys Glu Trp Gly Pro Arg Ser Thr Pro Ser Leu Thr Thr
218 110      115      120      125
220 Lys Ala Val Leu Leu Val Arg Lys Phe Gln Asn Ser Pro Ala Glu Asp
221      130      135      140
223 Phe Gln Glu Pro Cys Gln Tyr Ser Gln Glu Ser Gln Lys Phe Ser Cys
224      145      150      155
226 Gln Leu Ala Val Pro Glu Gly Asp Ser Ser Phe Tyr Ile Val Ser Met
227      160      165      170
229 Cys Val Ala Ser Ser Val Gly Ser Lys Phe Ser Lys Thr Gln Thr Phe
230      175      180      185
232 Gln Gly Cys Gly Ile Leu Gln Pro Asp Pro Pro Ala Asn Ile Thr Val
233 190      195      200      205
235 Thr Ala Val Ala Arg Asn Pro Arg Trp Leu Ser Val Thr Trp Gln Asp
236      210      215      220
238 Pro His Ser Trp Asn Ser Ser Phe Tyr Arg Leu Arg Phe Glu Leu Arg
239      225      230      235
241 Tyr Arg Ala Glu Arg Ser Lys Thr Phe Thr Thr Trp Met Val Lys Asp
242      240      245      250
244 Leu Gln His His Cys Val Ile His Asp Ala Trp Ser Gly Leu Arg His
245      255      260      265
247 Val Val Gln Leu Arg Ala Gln Glu Glu Phe Gly Gln Gly Glu Trp Ser
248 270      275      280      285
250 Glu Trp Ser Pro Glu Ala Met Gly Thr Pro Trp Thr Glu Ser Arg Ser
251      290      295      300
253 Pro Pro Ala Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
254      305      310      315
256 Gly Gly Ser Val Glu Pro Val Pro Pro Gly Glu Asp Ser Lys Asp Val
257      320      325      330
259 Ala Ala Pro His Arg Gln Pro Leu Thr Ser Ser Glu Arg Ile Asp Lys
260      335      340      345
262 Gln Ile Arg Tyr Ile Leu Asp Gly Ile Ser Ala Leu Arg Lys Glu Thr
263 350      355      360      365
265 Cys Asn Lys Ser Asn Met Cys Glu Ser Ser Lys Glu Ala Leu Ala Glu
266      370      375      380
268 Asn Asn Leu Asn Leu Pro Lys Met Ala Glu Lys Asp Gly Cys Phe Gln

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269          385          390          395
271 Ser Gly Phe Asn Glu Glu Thr Cys Leu Val Lys Ile Ile Thr Gly Leu
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274 Leu Glu Phe Glu Val Tyr Leu Glu Tyr Leu Gln Asn Arg Phe Glu Ser
275          415          420          425
277 Ser Glu Glu Gln Ala Arg Ala Val Gln Met Ser Thr Lys Val Leu Ile
278 430          435          440          445
280 Gln Phe Leu Gln Lys Lys Ala Lys Asn Leu Asp Ala Ile Thr Thr Pro
281          450          455          460
283 Asp Pro Thr Thr Asn Ala Ser Leu Leu Thr Lys Leu Gln Ala Gln Asn
284          465          470          475
286 Gln Trp Leu Gln Asp Met Thr Thr His Leu Ile Leu Arg Ser Phe Lys
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296 <213> ORGANISM: Unknown
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299 <221> NAME/KEY: sig_peptide
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303 <221> NAME/KEY: CDS
304 <222> LOCATION: (34)..(1593)
306 <220> FEATURE:
307 <221> NAME/KEY: mat_peptide
308 <222> LOCATION: (91)..(1593)
310 <220> FEATURE:
311 <223> OTHER INFORMATION: Description of Unknown Organism:A conjugate
312 comprising two polypeptides with a mutual
313 affinity.
315 <400> SEQUENCE: 3
316 gtcgacgcat ggagtggtag ccgaggagga agc atg ctg gcc gtc ggc tgc gcg 54
317          Met Leu Ala Val Gly Cys Ala
318          -15
320 ctg ctg gct gcc ctg ctg gcc gcg ccg gga gcg gcg ctg gcc cca agg 102
321 Leu Leu Ala Ala Leu Leu Ala Ala Pro Gly Ala Ala Leu Ala Pro Arg
322          -10          -5          -1 1
324 cgc tgc cct gcg cag gag gtg gca aga ggc gtg ctg acc agt ctg cca 150
325 Arg Cys Pro Ala Gln Glu Val Ala Arg Gly Val Leu Thr Ser Leu Pro
326 5          10          15          20
328 gga gac agc gtg act ctg acc tgc ccg ggg gta gag ccg gaa gac aat 198
329 Gly Asp Ser Val Thr Leu Thr Cys Pro Gly Val Glu Pro Glu Asp Asn
330          25          30          35
332 gcc act gtt cac tgg gtg ctc agg aag ccg gct gca ggc tcc cac ccc 246
333 Ala Thr Val His Trp Val Leu Arg Lys Pro Ala Ala Gly Ser His Pro
334          40          45          50
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**VERIFICATION SUMMARY**

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